



IFWO

RAW SEQUENCE LISTING

DATE: 09/01/2004

PATENT APPLICATION: US/10/787,378

TIME: 11:53:42

Input Set : N:\Crif3\RULE60\10787378.raw

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1 <110> APPLICANT: LEUNG, Shui-on
 2 HANSEN, Hans
 3 QU, Zhengxing
 4 <120> TITLE OF INVENTION: GLYCOSYLATED HUMANIZED B-CELL SPECIFIC ANTIBODIES
 5 <130> FILE REFERENCE: 018733/1049
 6 <140> CURRENT APPLICATION NUMBER: US/10/787,378
 7 <141> CURRENT FILING DATE: 2004-02-27
 8 <150> PRIOR APPLICATION NUMBER: US/09/894,839
 9 <151> PRIOR FILING DATE: 2001-06-29
 10 <150> PRIOR APPLICATION NUMBER: US 09/155,107
 11 <151> PRIOR FILING DATE: 1998-11-17
 12 <150> PRIOR APPLICATION NUMBER: US 60/013,709
 13 <151> PRIOR FILING DATE: 1996-03-20
 14 <160> NUMBER OF SEQ ID NOS: 47
 15 <170> SOFTWARE: PatentIn version 3.1
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 19 <212> TYPE: DNA
 20 <213> ORGANISM: Murinae gen. sp.
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 23 <222> LOCATION: (1)..(339)
 24 <223> OTHER INFORMATION:

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 27 Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ala Val Ser Ala Gly
 28 1 5 10 15
 29 gaa aac gtc act atg agc tgt aag tcc agt caa agt gtt tta tac agt 96
 30 Glu Asn Val Thr Met Ser Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
 31 20 25 30
 32 gca aat cac aag aac tac ttg gcc tgg tac cag cag aaa cca ggg cag 144
 33 Ala Asn His Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
 34 35 40 45
 35 tct cct aaa ctg ctg atc tac tgg gca tcc act agg gaa tct ggt gtc 192
 36 Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
 37 50 55 60
 38 cct gat cgc ttc aca ggc agc gga tct ggg aca gat ttt act ctt acc 240
 39 Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 40 65 70 75 80
 41 atc agc aga gta caa gtt gaa gac ctg gca att tat tat tgt cac caa 288
 42 Ile Ser Arg Val Gln Val Glu Asp Leu Ala Ile Tyr Tyr Cys His Gln
 43 85 90 95
 44 tac ctc tcc tgg acg ttc ggt gga ggg acc aag ctg gag atc aaa 336

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45     Tyr Leu Ser Ser Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
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47     cgt
48     Arg
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51 <211> LENGTH: 113
52 <212> TYPE: PRT
53 <213> ORGANISM: Murinae gen. sp.
54 <400> SEQUENCE: 2
55     Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ala Val Ser Ala Gly
56     1           5           10           15
57     Glu Asn Val Thr Met Ser Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
58           20           25           30
59     Ala Asn His Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
60           35           40           45
61     Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
62           50           55           60
63     Pro Asp Arg Phe Thr Gly Ser Gly Thr Asp Phe Thr Leu Thr
64           65           70           75           80
65     Ile Ser Arg Val Gln Val Glu Asp Leu Ala Ile Tyr Tyr Cys His Gln
66           85           90           95
67     Tyr Leu Ser Ser Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
68           100           105           110
69     Arg
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75 <220> FEATURE:
76 <221> NAME/KEY: CDS
77 <222> LOCATION: (1)..(348)
78 <223> OTHER INFORMATION:
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81     Gln Val Gln Leu Gln Glu Ser Gly Ala Glu Leu Ser Lys Pro Gly Ala
82     1           5           10           15
83     tca gtg aag atg tcc tgc aag gct tct ggc tac acc ttt act agc tac
84     Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
85           20           25           30
86     tgg ctg cac tgg ata aaa cag agg cct gga cag ggt ctg gaa tgg att
87     Trp Leu His Trp Ile Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
88           35           40           45
89     gga tac att aat cct agg aat gat tat act gag tac aat cag aac ttc
90     Gly Tyr Ile Asn Pro Arg Asn Asp Tyr Thr Glu Tyr Asn Gln Asn Phe
91           50           55           60
92     aag gac aag gcc aca ttg act gca gac aaa tcc tcc agc aca gcc tac
93     Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
94           65           70           75           80
95     atg caa ctg agc agc ctg aca tct gag gac tct gca gtc tat tac tgt

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96      Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
97              85              90              95
98      gca aga agg gat att act acg ttc tac tgg ggc caa ggc acc act ctc      336
99      Ala Arg Arg Asp Ile Thr Thr Phe Tyr Trp Gly Gln Gly Thr Thr Leu
100              100              105              110
101      aca gtc tcc tcg      348
102      Thr Val Ser Ser
103              115
105 <210> SEQ ID NO: 4
106 <211> LENGTH: 116
107 <212> TYPE: PRT
108 <213> ORGANISM: Murinae gen. sp.
109 <400> SEQUENCE: 4
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112      Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
113              20              25              30
114      Trp Leu His Trp Ile Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
115              35              40              45
116      Gly Tyr Ile Asn Pro Arg Asn Asp Tyr Thr Glu Tyr Asn Gln Asn Phe
117              50              55              60
118      Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
119      65              70              75              80
120      Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
121              85              90              95
122      Ala Arg Arg Asp Ile Thr Thr Phe Tyr Trp Gly Gln Gly Thr Thr Leu
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138      1              5              10              15
139      gat agg gtc act atg agc tgt aag tcc agt caa agt gtt tta tac agt      96
140      Asp Arg Val Thr Met Ser Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
141              20              25              30
142      gca aat cac aag aac tac ttg gcc tgg tac cag cag aaa cca ggg aaa      144
143      Ala Asn His Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
144              35              40              45
145      gca cct aaa ctg ctg atc tac tgg gca tcc act agg gaa tct ggt gtc      192
146      Ala Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val

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147          50          55          60
148 cct tcg cga ttc tct ggc agc gga tct ggg aca gat ttt act ttc acc      240
149 Pro Ser Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr
150 65          70          75          80
151 atc agc tct ctt caa cca gaa gac att gca aca tat tat tgt cac caa      288
152 Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys His Gln
153          85          90          95
154 tac ctc tcc tcg tgg acg ttc ggt gga ggg acc aag gtg cag atc aaa      336
155 Tyr Leu Ser Ser Trp Thr Phe Gly Gly Gly Thr Lys Val Gln Ile Lys
156          100          105          110
157 cgt      339
158 Arg
160 <210> SEQ ID NO: 6
161 <211> LENGTH: 113
162 <212> TYPE: PRT
163 <213> ORGANISM: Homo sapiens
164 <400> SEQUENCE: 6
165 Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
166 1          5          10          15
167 Asp Arg Val Thr Met Ser Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
168          20          25          30
169 Ala Asn His Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
170          35          40          45
171 Ala Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
172          50          55          60
173 Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr
174 65          70          75          80
175 Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys His Gln
176          85          90          95
177 Tyr Leu Ser Ser Trp Thr Phe Gly Gly Gly Thr Lys Val Gln Ile Lys
178          100          105          110
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182 <211> LENGTH: 348
183 <212> TYPE: DNA
184 <213> ORGANISM: Homo sapiens
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187 <222> LOCATION: (1)..(348)
188 <223> OTHER INFORMATION:
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192 1          5          10          15
193 tca gtg aag gtc tcc tgc aag gct tct ggc tac acc ttt act agc tac      96
194 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
195          20          25          30
196 tgg ctg cac tgg gtc agg cag gca cct gga cag ggt ctg gaa tgg att      144
197 Trp Leu His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile

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198          35          40          45
199 gga tac att aat cct agg aat gat tat act gag tac aat cag aac ttc      192
200 Gly Tyr Ile Asn Pro Arg Asn Asp Tyr Thr Glu Tyr Asn Gln Asn Phe
201          50          55          60
202 aag gac aag gcc aca ata act gca gac gaa tcc acc aat aca gcc tac      240
203 Lys Asp Lys Ala Thr Ile Thr Ala Asp Glu Ser Thr Asn Thr Ala Tyr
204 65          70          75          80
205 atg gag ctg agc agc ctg agg tct gag gac acg gca ttt tat ttt tgt      288
206 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Phe Tyr Phe Cys
207          85          90          95
208 gca aga agg gat att act acg ttc tac tgg ggc caa ggc acc acg gtc      336
209 Ala Arg Arg Asp Ile Thr Thr Phe Tyr Trp Gly Gln Gly Thr Thr Val
210          100          105          110
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212 Thr Val Ser Ser
213          115
215 <210> SEQ ID NO: 8
216 <211> LENGTH: 116
217 <212> TYPE: PRT
218 <213> ORGANISM: Homo sapiens
219 <400> SEQUENCE: 8
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221 1          5          10          15
222 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
223          20          25          30
224 Trp Leu His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
225          35          40          45
226 Gly Tyr Ile Asn Pro Arg Asn Asp Tyr Thr Glu Tyr Asn Gln Asn Phe
227          50          55          60
228 Lys Asp Lys Ala Thr Ile Thr Ala Asp Glu Ser Thr Asn Thr Ala Tyr
229 65          70          75          80
230 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Phe Tyr Phe Cys
231          85          90          95
232 Ala Arg Arg Asp Ile Thr Thr Phe Tyr Trp Gly Gln Gly Thr Thr Val
233          100          105          110
234 Thr Val Ser Ser
235          115
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239 <212> TYPE: PRT
240 <213> ORGANISM: Homo sapiens
241 <400> SEQUENCE: 9
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243 1          5          10          15
244 Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
245          20          25          30
246 Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
247          35          40          45
248 Ile

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/787,378

DATE: 09/01/2004

TIME: 11:53:43

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L:135 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:0
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